

PCT09

RAW SEQUENCE LISTING

DATE: 08/01/2001

PATENT APPLICATION: US/09/763,535

TIME: 18:42:56

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\08012001\I763535.raw

4 <110> APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
5 ROUSSEAU, GUY
6 LEMAIGRE, FREDRIC
8 <120> TITLE OF INVENTION: PHARMACEAUTICLA COMPOSITION FOR TREATING
9 OR PREVENTING DIABETES OR CANCER, OR THE WAARDENBURG
10 SYNDROME
12 <130> FILE REFERENCE: DECLE26.001APC
14 <140> CURRENT APPLICATION NUMBER: US 09/763,535
15 <141> CURRENT FILING DATE: 2001-02-20
17 <150> PRIOR APPLICATION NUMBER: BE 9800609
18 <151> PRIOR FILING DATE: 1998-08-17
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1655
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
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31 gcctcaccaa agacctagaa cgtgcgccat gaacccggag ctgacaatgg aaagtctggg 120
32 cactttgcac ggcgcgcgcg gcggcggcag tggcgggggc ggcggcgggg gcggcggggg 180
33 cggcgcgcgg ggcgcgggcc atgagcagga gctgctggcc agccccagcc cccaccacgc 240
34 gcgcgcgcgg ccgcgtggct cgtgcggggg ccctccgcgc cctccaaccg cgcaccagga 300
35 gctgggcacg gcggcagcgg gcgcagcggc ggcgctgcgc tcggccatgg tcaccagcat 360
36 ggccctcgatc ctggacggcg gcgactaccg gcccgagctc tccatccgcg tgcaccacgc 420
37 catgagcatg tctgcgact cgtctccgcc tggcatgggc atgagcaaca cctacaccac 480
38 gctgacaccg ctccagccgc tgccacccat ctccaccgtg tctgacaagt tccaccaccc 540
39 tcaccgcgac accattccgc accaccacca ccaccaccac caccagcgcc tgtccggcaa 600
40 cgtcagcgcc agcttcaccc tcatgcgcga cgagcgcggg ctcccgggcc tgaacaacct 660
41 ctacagtccc tacaaggaga tgcccggcat gagccagagc ctgtccccgc tggccggcac 720
42 gccgctgggc aacgggctag gcggcctcca caacgcgcag cagagtctgc ccaactacgg 780
43 tccgcccggc cagacaaaa tgctcagccc caacttcgac gcgcaccaca ctgccatgct 840
44 gaccgcgggt gagcaacacc tgtcccgcgg cctgggcacc ccacctgcgg ccatgatgtc 900
45 gcacctgaac ggctgcacc acccggggcca cactcagtct caccggccgg tgctggcacc 960
46 cagtcgcgag cgccaccct cgtcctcctc gggctcgcag gtggccacgt cgggccagct 1020
47 ggaagaaatc aacaccaaag aggtggccca gcgcataca gcggagctga agcgctacag 1080
48 tatccccag gcgatctttg cgcagagggg gctgtgcccg tctcagggga ctctctccga 1140
49 cctgctccgg aatccaaaac cgtggagtaa actcaaactt ggcagggaga ccttcgcgag 1200
50 gatgtggaag tggcttcagg agcccagatt ccagcgcgat tccgccttac gcctggcagc 1260
51 gtgcaaacgc aaagagcaag aaccaaacaa agacaggaac aattcccaga agaagtcccg 1320
52 cctggtgttc actgacctcc aacgccgaac actcttcgcc atcttcaagg agaacaaacg 1380
53 cccgtcaaag gagatgcaga tcaccatttc ccagcagctg ggccctggagc tcacaaccgt 1440
54 cagcaacttc ttcatgaacg cccggcgccg cagcctggag aagtggcaag acgatctgag 1500
55 cacagggggc tctcgtcca cctccagcac gtgtacaaa gcatgatgga aggactctca 1560
56 cttgggcaca agtcacctcc aaatgaggac aacagatacc aaaagaaaac aaaggaaaaa 1620
57 gacaccggat tcctagctgg ggccctgcac tgggtg 1655
59 <210> SEQ ID NO: 2

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60 <211> LENGTH: 485
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
65 Met Asn Pro Glu Leu Thr Met Glu Ser Leu Gly Thr Leu His Gly Ala
66 1 5 10 15
67 Arg Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
68 20 25 30
69 Gly Gly Gly Pro Gly His Glu Gln Leu Leu Ala Ser Pro Ser Pro
70 35 40 45
71 His His Ala Arg Arg Gly Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro
72 50 55 60
73 Pro Pro Thr Ala His Gln Glu Leu Gly Thr Ala Ala Ala Ala Ala Ala
74 65 70 75 80
75 Ala Ala Ser Arg Ser Ala Met Val Thr Ser Met Ala Ser Ile Leu Asp
76 85 90 95
77 Gly Gly Asp Tyr Arg Pro Glu Leu Ser Ile Pro Leu His His Ala Met
78 100 105 110
79 Ser Met Ser Cys Asp Ser Ser Pro Pro Gly Met Gly Met Ser Asn Thr
80 115 120 125
81 Tyr Thr Thr Leu Thr Pro Leu Gln Pro Leu Pro Pro Ile Ser Thr Val
82 130 135 140
83 Ser Asp Lys Phe His His Pro His Pro His His Pro His His His
84 145 150 155 160
85 His His His His His Gln Arg Leu Ser Gly Asn Val Ser Gly Ser Phe
86 165 170 175
87 Thr Leu Met Arg Asp Glu Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr
88 180 185 190
89 Ser Pro Tyr Lys Glu Met Pro Gly Met Ser Gln Ser Leu Ser Pro Leu
90 195 200 205
91 Ala Ala Thr Pro Leu Gly Asn Gly Leu Gly Gly Leu His Asn Ala Gln
92 210 215 220
93 Gln Ser Leu Pro Asn Tyr Gly Pro Pro Gly His Asp Lys Met Leu Ser
94 225 230 235 240
95 Pro Asn Phe Asp Ala His His Thr Ala Met Leu Thr Arg Gly Glu Gln
96 245 250 255
97 His Leu Ser Arg Gly Leu Gly Thr Pro Pro Ala Ala Met Met Ser His
98 260 265 270
99 Leu Asn Gly Leu His His Pro Gly His Thr Gln Ser His Gly Pro Val
100 275 280 285
101 Leu Ala Pro Ser Arg Glu Arg Pro Pro Ser Ser Ser Ser Gly Ser Gln
102 290 295 300
103 Val Ala Thr Ser Gly Gln Leu Glu Glu Ile Asn Thr Lys Glu Val Ala
104 305 310 315 320
105 Gln Arg Ile Thr Ala Glu Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile
106 325 330 335
107 Phe Ala Gln Arg Val Leu Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu
108 340 345 350
109 Leu Arg Asn Pro Lys Pro Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr

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110          355          360          365
111 Phe Arg Arg Met Trp Lys Trp Leu Gln Glu Pro Glu Phe Gln Arg Met
112          370          375          380
113 Ser Ala Leu Arg Leu Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn
114 385          390          395          400
115 Lys Asp Arg Asn Asn Ser Gln Lys Lys Ser Arg Leu Val Phe Thr Asp
116          405          410          415
117 Leu Gln Arg Arg Thr Leu Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro
118          420          425          430
119 Ser Lys Glu Met Gln Ile Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu
120          435          440          445
121 Thr Thr Val Ser Asn Phe Phe Met Asn Ala Arg Arg Arg Ser Leu Glu
122          450          455          460
123 Lys Trp Gln Asp Asp Leu Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser
124 465          470          475          480
125 Thr Cys Thr Lys Ala
126          485
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 1485
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 3
135 atggagctga gcttggagag cctgggggggc ctgcacacgc tggcccacgc gcaggcgggc 60
136 gagctgctga gcccgggcca cgcgcgctcg gcggcggcgc agcacgcggc cctggtggcg 120
137 cccggggcgc cgggcctggt ggccggcatg gcgagcctgc tggacggcgg cggcgggcgc 180
138 ggcggtgggg gcgcccgggg cgcgggcggc gcgggcagcg cggcgggcgg cgcggacttc 240
139 cgcggggaac tggcgggccc gctgcacccc gcaatgggca tggcctgcga ggcgcccggc 300
140 ctgggcggca cctacacgac gctcacgccc ctgcagcacc tgcgcgcgct cgcggccgtg 360
141 gccgacaagt tccaccagca cgcggcgggc gcggccgtgg ccggggcgca cggcgggccat 420
142 cccacgcgc acccgacccc ggcggccgcg ccgccccgc caccocgcgc gcagcgtctg 480
143 gcggccagcg tgagcggcag ctacacccctc atgcgcgacg agcggggcgg gctcgcctcc 540
144 gtgggccacc tctacggacc ctacggcaag gagctgcccg ccatggggtc gccgtgtctg 600
145 ccgctgcccc acgcgctgcc gcccgcgctg cacggcgccc cgcagccccc gccgcggcca 660
146 ccacccccgc cgctggccgc ctacggcccc ccaggccacc tggctgggga caagctgctg 720
147 ccgcccgcgc ccttcgagcc gcacgccgcg ctgctgggac gcgcggagga cgcactggcc 780
148 cgcgggctgc ccggaggcgg cgcgggcaca ggcagcggcg gagcgggcag cgggagcgcc 840
149 gcggggctgc tggcgcgctt ggcgggctg gcggcgggcg gggcgcacgg gccgcaggag 900
150 ggaggcggcg gcccggcgcg gagcggcgcg ggcgccagcg cggcgcgagc ggcggaggag 960
151 atcaacacca aggaggtggc gcagcgcctc acggcgggag tgaagcgcta cagcatcccg 1020
152 caggcaatct tcgcgcagcg gatcctgtgt cgctctcagg gcacgctctc cgacctgctg 1080
153 cgcaaccccc agcgtgggag caagctcaaa tccggccgcg agaccttcgc caggatgtgg 1140
154 aagtggctgc aggagccaga gttccagcgc atgtcggcgc tgcgcttggc agcgtgcaag 1200
155 cgcaaggaac aggagcagca gaaggagcgc gccctgcagc ccaagaagca gcgcctggtg 1260
156 ttcaccgacc tgcagcgacg cacgctgacg gccatcttca aggagaacaa gcggccgtcc 1320
157 aaggagatgc aggtcaccat ctgcagcagc ctcggttggc agctcaacac cgtcagcaac 1380
158 ttcttcatga acgcgcggcg ccgctgcatg aaccgctggg ctgaggagcc cagcacggcc 1440
159 cccgggggccc ccgcggcgcg cacggccact ttctccaagg cctga 1485
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 494

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163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 4
167 Met Glu Leu Ser Leu Glu Ser Leu Gly Gly Leu His Ser Val Ala His
168 1 5 10 15
169 Ala Gln Ala Gly Glu Leu Leu Ser Pro Gly His Ala Arg Ser Ala Ala
170 20 25 30
171 Ala Gln His Arg Gly Leu Val Ala Pro Gly Arg Pro Gly Leu Val Ala
172 35 40 45
173 Gly Met Ala Ser Leu Leu Asp Gly Gly Gly Gly Gly Gly Gly Gly
174 50 55 60
175 Ala Gly Gly Ala Gly Gly Ala Gly Ser Ala Gly Gly Gly Ala Asp Phe
176 65 70 75 80
177 Arg Gly Glu Leu Ala Gly Pro Leu His Pro Ala Met Gly Met Ala Cys
178 85 90 95
179 Glu Ala Pro Gly Leu Gly Gly Thr Tyr Thr Thr Leu Thr Pro Leu Gln
180 100 105 110
181 His Leu Pro Pro Leu Ala Ala Val Ala Asp Lys Phe His Gln His Ala
182 115 120 125
183 Ala Ala Ala Ala Val Ala Gly Ala His Gly Gly His Pro His Ala His
184 130 135 140
185 Pro His Pro Ala Ala Ala Pro Pro Pro Pro Pro Pro Gln Arg Leu
186 145 150 155 160
187 Ala Ala Ser Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu Arg Ala
188 165 170 175
189 Ala Leu Ala Ser Val Gly His Leu Tyr Gly Pro Tyr Gly Lys Glu Leu
190 180 185 190
191 Pro Ala Met Gly Ser Pro Leu Ser Pro Leu Pro Asn Ala Leu Pro Pro
192 195 200 205
193 Ala Leu His Gly Ala Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro
194 210 215 220
195 Leu Ala Ala Tyr Gly Pro Pro Gly His Leu Ala Gly Asp Lys Leu Leu
196 225 230 235 240
197 Pro Pro Ala Ala Phe Glu Pro His Ala Ala Leu Leu Gly Arg Ala Glu
198 245 250 255
199 Asp Ala Leu Ala Arg Gly Leu Pro Gly Gly Gly Gly Gly Thr Gly Ser
200 260 265 270
201 Gly Gly Ala Gly Ser Gly Ser Ala Ala Gly Leu Leu Ala Pro Leu Gly
202 275 280 285
203 Gly Leu Ala Ala Ala Gly Ala His Gly Pro His Gly Gly Gly Gly Gly
204 290 295 300
205 Pro Gly Gly Ser Gly Gly Gly Pro Ser Ala Gly Ala Ala Ala Glu Glu
206 305 310 315 320
207 Ile Asn Thr Lys Glu Val Ala Gln Arg Ile Thr Ala Glu Leu Lys Arg
208 325 330 335
209 Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Ile Leu Cys Arg Ser
210 340 345 350
211 Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro Trp Ser Lys
212 355 360 365

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```

213 Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys Trp Leu Gln
214      370                      375                      380
215 Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala Ala Cys Lys
216 385                      390                      395                      400
217 Arg Lys Glu Gln Glu Gln Gln Lys Glu Arg Ala Leu Gln Pro Lys Lys
218                      405                      410                      415
219 Gln Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu Ile Ala Ile
220                      420                      425                      430
221 Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Val Thr Ile Ser
222                      435                      440                      445
223 Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn
224      450                      455                      460
225 Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala
226 465                      470                      475                      480
227 Pro Gly Gly Pro Ala Gly Ala Thr Ala Thr Phe Ser Lys Ala
228                      485                      490

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VERIFICATION SUMMARY

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